

## SEQUENCE LISTING

### (1) GENERAL INFORMATION

- (i) APPLICANT:  
Seidel, Christoph; Weinhues, Ursula-Henrike;  
Schmitt, Urban; Motz, Manfred; Wiedmann, Michael;  
Upmeier, Barbara; Soutscheck, Erwin
- (ii) TITLE OF INVENTION:  
Recombinant antigen from the NS3 region of the hepatitis C virus
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Felfe & Lynch  
(B) STREET: 805 Third Avenue  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: USA  
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
(B) COMPUTER: IBM PS/2  
(C) OPERATING SYSTEM: PC-DOS  
(D) SOFTWARE: PatentIn Release #1.0,  
Version #1.25 (EPA)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/511,759  
(B) FILING DATE: 7-AUGUST-1995y
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: p 44 28 705.4  
(B) FILING DATE: 12 AUGUST 1994
- (viii) ATTORNEY/AGENT INFORMATION  
(A) NAME: HANSON, NORMAN  
(B) REGISTRATION NUMBER: 30, 946  
(C) REFERENCE/DOCKET NUMBER: HUBR 1067.1
- (ix) TELECOMMUNICATION INFORMATION  
(A) TELEPHONE: 212-688-9200  
(B) TELEFAX: 212-838-3884

106290-2299860

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 885 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: both  
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) INITIAL ORIGIN:  
    (A) ORGANISM: hepatitis C virus
- (viii) POSITION IN GENOME:  
    (A) CHROMOSOME SEGMENT: NS3
- (ix) CHARACTERISTICS:  
    (A) NAME/KEY: CDS  
    (B) LOCATION: 1..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG ACC ATG ATT ACG AAT TCC CGG GGA TCC ATC ATG AAA TCC CCG GTG 48  
Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val  
1 5 10 15

TTC ACG GAT AAC TCC TCT CCA CCG GTA GTG CCC CAG AGC TTC CAG GTG 96  
Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val  
20 25 30

GCT CAC CTG CAT GCT CCC ACA GGC AGC GGC AAG AGC ACC AAG GTC CCG 144  
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro  
35 40 45

GCT GCA TAC GCA GCT CAG GGC TAC AAG GTG CTA GTG CTC AAC CCT TCT 192  
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser  
50 55 60

GTT GCT GCA ACA TTG GGC TTT GGT GCC TAC ATG TCC AAG GCT CAT GGG 240  
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly  
65 70 75 80

ATC GAT CCT AAC ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT GGC AGC 288  
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser  
85 90 95

CCC ATT ACG TAC TCC ACT TAC GGC AAG TTT CTT GCC GAC GGC GGG TGC 336  
Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys  
100 105 110

[illegible]

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val  
1 5 10 15  
Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val  
20 25 30  
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro  
35 40 45  
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser  
50 55 60  
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly  
65 70 75 80  
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser  
85 90 95  
Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys  
100 105 110  
Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr  
115 120 125  
Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu  
130 135 140  
Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly  
145 150 155 160  
Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr  
165 170 175  
Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile  
180 185 190  
Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp  
195 200 205

Glu Leu Ala Thr Lys Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr  
 210 215 220  
 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val  
 225 230 235 240  
 Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp  
 245 250 255  
 Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser  
 260 265 270  
 Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala  
 275 280 285  
 Val Ser Arg Thr Gln Arg Arg  
 290 295

(4) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT

40

(5) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCGGGAGAC

(6) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GAGGGATCCA TCATGAAAGC GGTGGACTTT ATCCCTGTG

39

(7) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GAGAAGCTTT TAACACGTGT TGCAGTCTAT CAC

33

(8) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GAGGGATCCA TCATGAAACA CCTGCATGCT CCCACCGGC

39

1062990-2E095B50



Asp Gly Gly Cys	Ala Gly Gly Ala Tyr	Asp Ile Ile Ile Cys	Asp
110		115	120
Glu Cys His Ser	Thr Asp Ala Thr Ser	Ile Leu Gly Ile Gly	Thr
125		130	135
Val Leu Asp Gln	Gly Glu Thr Ala Gly	Ala Lys Leu Val Val	Phe
140		145	150
Ala Thr Ala Thr	Pro Pro Gly Ser Val	Thr Val Pro His Pro	Asn
155		160	165
Ile Glu Glu Val	Ala Leu Ser Thr Thr	Gly Glu Ile Pro Phe	Tyr
170		175	180
Gly Lys Ala Ile	Pro Leu Glu Val Ile	Lys Gly Gly Arg His	Leu
185		190	195
Ile Phe Cys His	Ser Lys Arg Lys Cys	Asp Glu Leu Ala Thr	Lys
200		205	210
Leu Val Ala Met	Gly Ile Asn Ala Val	Ala Tyr Tyr Arg Gly	Leu
215		220	225
Asp Val Ser Val	Ile Pro Thr Ser Gly	Asp Val Val Val Val	Ala
230		235	240
Thr Asp Ala Leu	Met Thr Gly Tyr Thr	Gly Asp Phe Asp Ser	Val
245		250	255
Ile Asp Cys Asn	Thr Cys Val Thr Gln	Thr Val Asp Phe Ser	Leu
260		265	270
Asp Pro Thr Phe	Thr Ile Glu Thr Thr	Thr Leu Pro Gln Asp	Ala
275		280	285
Val Ser Arg Thr	Gln Arg Arg Gly Arg	Thr Gly Arg Gly Lys	Pro
290		295	300

Gly Ile  
302



SEQUENCE PROTOCOL

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Boehringer Mannheim GmbH
- (B) ROAD: Sandhofer Str. 112-132
- (C) CITY: Mannheim
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 68305

(ii) TITLE OF APPLICATION: Recombinant antigen from  
the NS3 region of the hepatitis C virus

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0,  
Version #1.25 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: both
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

09896032-062901

(vi) INITIAL ORIGIN:

(A) ORGANISM: hepatitis c virus

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: NS3

(ix) CHARACTERISTICS:

(A) NAME/KEY: CDS

(B) LOCATION: 1..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG ACC ATG ATT ACG AAT TCC CGG GGA TCC ATC ATG AAA TCC CCG GTG	48
Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val	
1 5 10 15	
TTC ACG GAT AAC TCC TCT CCA CCG GTA GTG CCC CAG AGC TTC CAG GTG	96
Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val	
20 25 30	
GCT CAC CTG CAT GCT CCC ACA GGC AGC GGC AAG AGC ACC AAG GTC CCG	144
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro	
35 40 45	
GCT GCA TAC GCA GCT CAG GGC TAC AAG GTG CTA GTG CTC AAC CCT TCT	192
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser	
50 55 60	
GTT GCT GCA ACA TTG GGC TTT GGT GCC TAC ATG TCC AAG GCT CAT GGG	240
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly	
65 70 75 80	
ATC GAT CCT AAC ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT GGC AGC	288
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser	
85 90 95	
CCC ATT ACG TAC TCC ACT TAC GGC AAG TTT CTT GCC GAC GGC GGG TGC	336
Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys	
100 105 110	
GCA GGG GGT GCT TAT GAC ATA ATA ATT TGT GAC GAG TGC CAC TCC ACG	384
Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
115 120 125	
GAT GCC ACA TCC ATC TTG GGC ATC GGC ACT GTC CTT GAC CAA GGA GAG	432
Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu	
130 135 140	

ACT	GCG	GGG	GCG	AAA	Leu	Val	Val	Phe	Ala	Thr	Ala	Thr	Pro	Pro	Gly	480
Thr	Ala	Gly	Ala	Lys	150											
145																
TCC	GTC	ACT	GTG	CCC	CAT	CCC	AAC	ATT	GAG	GAG	GTT	GCT	CTA	TCC	ACC	528
Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Thr	
				165					170					175		
ACC	GGA	GAG	ATC	CCT	TTT	TAC	GGC	AAG	GCT	ATC	CCC	CTT	GAG	GTA	ATC	576
Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Leu	Glu	Val	Ile	
			180					185					190			
AAG	GGG	GGG	AGA	CAT	CTC	ATC	TTC	TGT	CAT	TCA	AAG	AGG	AAG	TGC	GAT	624
Lys	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	Lys	Arg	Lys	Cys	Asp	
		195					200					205				
GAG	CTC	GCC	ACA	AAG	CTG	GTC	GCA	ATG	GGC	ATC	AAT	GCC	GTG	GCC	TAC	672
Glu	Leu	Ala	Thr	Lys	Leu	Val	Ala	Met	Gly	Ile	Asn	Ala	Val	Ala	Tyr	
	210					215					220					
TAC	CGC	GGT	CTT	GAC	GTG	TCC	GTC	ATC	CCG	ACC	AGC	GGT	GAT	GTT	GTC	720
Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	Thr	Ser	Gly	Asp	Val	Val	
225				230						235					240	
GTC	GTG	GCA	ACC	GAC	GCC	CTC	ATG	ACC	GGC	TAT	ACC	GGC	GAC	TTC	GAC	768
Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	
				245					250					255		
TGG	GTG	ATA	GAC	TGC	AAC	ACG	TGT	GTC	ACT	CAG	ACA	GTC	GAT	TTC	AGC	816
Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	
			260					265					270			
CTT	GAC	CCT	ACC	TTC	ACC	ATT	GAG	ACG	ACC	ACA	CTT	CCC	CAG	GAT	GCT	864
Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	Thr	Leu	Pro	Gln	Asp	Ala	
		275					280					285				
GTC	TCC	CGC	ACT	CAA	CGA	CGG										885
Val	Ser	Arg	Thr	Gln	Arg	Arg										
	290					295										

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val

1			5			10			15						
Phe	Thr	Asp	Asn 20	Ser	Ser	Pro	Pro	Val 25	Val	Pro	Gln	Ser	Phe 30	Gln	Val
Ala	His	Leu	His 35	Ala	Pro	Thr	Gly 40	Ser	Gly	Lys	Ser	Thr 45	Lys	Val	Pro
Ala	Ala 50	Tyr	Ala	Ala	Gln	Gly 55	Tyr	Lys	Val	Leu	Val 60	Leu	Asn	Pro	Ser
Val 65	Ala	Ala	Thr	Leu	Gly 70	Phe	Gly	Ala	Tyr	Met 75	Ser	Lys	Ala	His	Gly 80
Ile	Asp	Pro	Asn	Ile 85	Arg	Thr	Gly	Val	Arg 90	Thr	Ile	Thr	Thr	Gly 95	Ser
Pro	Ile	Thr	Tyr 100	Ser	Thr	Tyr	Gly	Lys 105	Phe	Leu	Ala	Asp	Gly 110	Gly	Cys
Ala	Gly	Gly 115	Ala	Tyr	Asp	Ile	Ile 120	Ile	Cys	Asp	Glu	Cys 125	His	Ser	Thr
Asp	Ala 130	Thr	Ser	Ile	Leu	Gly 135	Ile	Gly	Thr	Val	Leu 140	Asp	Gln	Gly	Glu
Thr 145	Ala	Gly	Ala	Lys	Leu 150	Val	Val	Phe	Ala	Thr 155	Ala	Thr	Pro	Pro	Gly 160
Ser	Val	Thr	Val	Pro 165	His	Pro	Asn	Ile	Glu 170	Glu	Val	Ala	Leu	Ser 175	Thr
Thr	Gly	Glu	Ile 180	Pro	Phe	Tyr	Gly	Lys 185	Ala	Ile	Pro	Leu	Glu 190	Val	Ile
Lys	Gly	Gly 195	Arg	His	Leu	Ile	Phe 200	Cys	His	Ser	Lys	Arg 205	Lys	Cys	Asp
Glu	Leu 210	Ala	Thr	Lys	Leu	Val 215	Ala	Met	Gly	Ile	Asn 220	Ala	Val	Ala	Tyr
Tyr 225	Arg	Gly	Leu	Asp	Val 230	Ser	Val	Ile	Pro	Thr 235	Ser	Gly	Asp	Val	Val 240
Val	Val	Ala	Thr	Asp 245	Ala	Leu	Met	Thr	Gly 250	Tyr	Thr	Gly	Asp	Phe 255	Asp
Ser	Val	Ile	Asp 260	Cys	Asn	Thr	Cys	Val 265	Thr	Gln	Thr	Val	Asp 270	Phe	Ser
Leu	Asp	Pro	Thr 275	Phe	Thr	Ile	Glu 280	Thr	Thr	Thr	Leu	Pro 285	Gln	Asp	Ala
Val	Ser	Arg	Thr	Gln	Arg	Arg 295									

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT

40

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCGGGAGAC

39

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: singl

09896032-062901

(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

GAGGGATCCA TCATGAAAGC GGTGGACTTT ATCCCTGTG

39

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRAND FORM: single

(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GAGAAGCTTT TAACACGTGT TGCAGTCTAT CAC

33

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRAND FORM: single

(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

0996032-062901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GAGGGATCCA TCATGAAACA CCTGCATGCT CCCACCGGC

39

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRAND FORM: single

(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

GAGAAGCTTT TAATACCAAG CACAGCCTGC GTC

33

090902-2E090800